

CLAIMS

1. Oligonucleotide for the specific identification of *Staphylococci* species which nucleotide sequence has between 15 and 45 base pairs, preferably between 15 and 25 base pairs, and which presents more than 60% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3.

2. Oligonucleotide according to claim 1 for the specific identification of *Staphylococci* species, which nucleotide sequence has between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which presents more than 70% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3.

3. Oligonucleotide according to claim 1 or 2 for the specific identification of *Staphylococci* species, which nucleotide sequence has between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which presents more than 80% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3.

4. Oligonucleotide according to any of the claims 1 to 3 for the specific identification of *Staphylococci* species, which nucleotide sequence has between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which presents more than 90% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3.

5. Oligonucleotide according to any of the preceding claims, which is selected from the group consisting of the following nucleotide sequences :

- ANAATGAANTTTACNAATTTNACNGCNANAGANTT

and more particularly TAATGAAGTTTACAAAATTT or TAATGAAGTTTACNAAATTT

Replaced
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- ATGNCNNANAGNCATTTNACNCANA
and more particularly TGCCATATAGTCATTTACGC
- TAGTNGGNATNAANAANAANNATAANGANGTNATTGC
- GTNCCNGTNATGAAANTNTTNAANTANTTTTATTC
- 5 - AATGCNCGNANGATTGG
- GNAANNGNAANACNAAAAAGTNNANAANAATGGNGTNAAAGT
and more particularly AAAAAGTTCAAAAAATGG and
AAAAAGTACAAAAATGG
- AAGANGANNTNCCNATNTTNGNTCATTNATGGANGATAC
- 10 - TATATNNANTTTGATGANTA ,
- AANGANATNGANAAANGNCCNGANAANAAAAA
and more particularly AAAGATATTGAAAAACGA,
AAAGATATTGAAAAGAGACC, AAAGATATCGAGAAAGAC and
AAAGACATCGACAAGCGT.
- 15 - ANCATGGNAANGAATTACCNAT
and more particularly GAACATGGTAATGAATTAC
- AATCCNTNTGAAGTNGTNTANTANGCNGGTGG
- AGNTATGCNNTNCAATGGNNNATGATTAANTATGC
- TTTANNGANGANGCNGAAGATGNNGGNGTNNTNAANTTNAAAAA
- 20 and more particularly TTTACTGAAGATGCTGAAGA
- GTTGGNGANTTNNTNAAACC
and more particularly GTTGGTGACTTTATTAAACC
- ATGAAATTTACAGAGTTAA

6. Oligonucleotide for the specific
25 identification of *Staphylococci* species which nucleotide
sequence has between 15 and 350 base pairs, preferably
between 17 and 250 base pairs, and which presents less than
50% homology with the "consensus" *femA* nucleotide sequence
(CNS) of Fig. 3.

30 7. Oligonucleotide according to claim 6 for
the specific identification of *Staphylococci* species which
nucleotide sequence has between 15 and 350 base pairs,

preferably between 17 and 250 base pairs, and which presents less than 40% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3.

8. Oligonucleotide according to claim 6 or 7
5 for the specific identification of *Staphylococci* species which nucleotide sequence has between 15 and 350 base pairs, preferably between 17 and 250 base pairs, and which presents less than 30% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3.

10 9. Oligonucleotide according to any of the claims 6 to 8 for the specific identification of *Staphylococci* species which nucleotide sequence has between 15 and 350 base pairs, preferably between 17 and 250 base pairs, and which presents less than 20% homology with the
15 "consensus" *femA* nucleotide sequence (CNS) of Fig. 3.

10. Oligonucleotide according to claim 6, being a primer which nucleotide sequence has between 15 and 45 base pairs, preferably between 17 and 25 base pairs.

11. Oligonucleotide according to claim 10,
20 which is selected from the group consisting of the following nucleotide sequences :

- ACAGCAGATGACATCATT
- TAATGAAAGAAATGTGCTTA
- ACACAACCTTCAATTAGAAC
- 25 - AGTATTAGCAAATGCGG
- ATGCATATTTTCCGTAA
- CAGCAGATGACATCATT
- CATCTAAAGATATATTAAATGGA
- AGTATTAGCAAATGCGGGTCAC
- 30 - CAACACAACCTTCAATTAGAA

12. Identification and/or quantification method of a *Staphylococci* species, which may present resistance to antibiotics and which is present in a sample, said method comprising the steps of :

- 5 - obtaining a nucleotide sequence from a *Staphylococci* species present in the sample,
- amplifying said nucleotide sequence with one or more oligonucleotide(s) according to the claims 1 to 8, and
- identifying and possibly quantifying the specific
10 *Staphylococci* species :
- by reverse hybridisation of the amplified nucleotide sequence with one or more oligonucleotide(s) according to the claims 9 to 11 which is (are) specific of said *Staphylococci*
15 species and is (are) immobilised on a solid support or
- by a comparative measure of the length of the amplified nucleotide sequence.

13. Diagnostic device for the identification
20 of *Staphylococci* species comprising the oligonucleotide according to any of the preceding claims 1 to 11 and possibly all the media necessary for the identification of an amplified sequence of said *Staphylococci* species through
25 of in situ hybridisation, hybridisation on a solid support, in solution on dot blot, Northern blot, Southern blot, probe hybridisation by the use of an isotopic or non-isotopic label, genetic amplification or a mixture thereof.

14. *femA* genetic sequence which presents more
30 than 90% homology with a nucleotide or amino acid sequence selected from the group consisting of the nucleotide or

amino acid sequences represented in the enclosed Fig. 6 to 13.

15. Genetic sequence according to claim 14, being the nucleotide sequence of Fig. 6.

5 16. Genetic sequence according to claim 14, being the amino acid sequence of Fig. 6.

17. Genetic sequence according to claim 14, being the nucleotide sequence of Fig. 7.

10 18. Genetic sequence according to claim 14, being the amino acid sequence, of Fig. 7.

19. Genetic sequence according to claim 14, being the nucleotide sequence of Fig. 8.

20. Genetic sequence according to claim 14, being the amino acid sequence of Fig. 8.

15 21. Genetic sequence according to claim 14, being the nucleotide sequence of Fig. 9.

22. Genetic sequence according to claim 14, being the amino acid sequence of Fig. 9.

20 23. Genetic sequence according to claim 14, being the nucleotide sequence of Fig. 10.

24. Genetic sequence according to claim 14, being the amino acid sequence of Fig. 10.

25. Genetic sequence according to claim 14, being the nucleotide sequence of Fig. 11.

25 26. Genetic sequence according to claim 14, being the amino acid sequence of Fig. 11.

27. Genetic sequence according to claim 14, being the nucleotide sequence of Fig. 12.

30 28. Genetic sequence according to claim 14, being the amino acid sequence of Fig. 12.

29. Genetic sequence according to claim 14, being the nucleotide sequence of Fig. 13.

30. Genetic sequence according to claim 14,
being the amino acid sequence of Fig. 13.